Attorney's Docket No. 12817-004001 / PH-581US-CIP

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	: Satoshi Yamamoto et al.	Art Unit	: Unknown
Serial No.	: 09/823,829	Examiner	: Unknown
Filed	: March 30, 2001		
Title	: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GYRASE GENE AS AN INDICATOR		

BOX SEQUENCE
U.S. Patent and Trademark Office
P.O. Box 2327
Arlington, VA 22202

PRELIMINARY AMENDMENT

Applicants submit herewith a Sequence Listing in computer readable form as required by 37 CFR §1.824. In addition, applicants submit a substitute Sequence Listing as required under 37 CFR §1.823(a) and a statement under 37 CFR §1.821(f).

Applicants respectfully request entry of the paper copy and computer readable copy of the Sequence Listing filed herewith for the instant application. Furthermore, applicants request entry of the following amendments.

In the specification:

Replace the original Sequence Listing with the substitute Sequence Listing filed herewith.

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the U.S. Patent and Trademark Office, P.O. Box 2327, Arlington, VA 22202.

March 8, 2002
Date of Deposit

Rose Paperth
Signature

Rose Paperth
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Replace the paragraph beginning at page 4, line 11 with the following rewritten paragraph:

--As described above, the present Inventors have already developed and applied successfully the method for the identification/classification or detection/monitoring of organisms using *gyr B* sequences. In this method, a *gyr B* gene fragment of an organism of interest is amplified by PCR using primers designed from the two amino acid sequences, His-Ala-Gly-Gly-Lys-Phe-Asp (SEQ ID NO:81) and Met-Thr-Asp-Ala-Asp-Val-Asp-Gly (SEQ ID NO:82), which are highly conserved among the GyrB sequences of many organisms. Subsequently, the amplified fragments are subjected to direct sequencing. Since the *gyr B* genes code for proteins, they have frequently undergone neutral mutations. Thus, the nucleotide sequence of the *gyr B* genes vary considerable even among related organisms. For this reason, the above method has been shown to be effective for discriminating organisms at a level of species of subspecies.--